

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

1. **(Currently amended)** A composition comprising an orthogonal glutamyl-tRNA (glutamyl O-tRNA) derived from one or more archaeal tRNAs, wherein the glutamyl O-tRNA comprises a polynucleotide sequence at least 8095% identical to SEQ ID NO.: 67, wherein the glutamyl O-tRNA comprises a G:C base pair at positions corresponding to 10:28;}

and wherein the glutamyl O-tRNA suppresses in the presence of a glutamyl tRNA synthetase derived from an RS selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosarcina mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase.

2. **(Cancelled)**

3. **(Currently amended)** The composition of claim 1, further comprising a wherein the selector codon that is an amber codon.

4. **(Currently amended)** The composition of claim 1, wherein the glutamyl O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 67, or and is transcribed from a complementary polynucleotide sequence thereof.

5. **(Currently amended)** The composition of claim 1, wherein the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid in response to thea selector codon.

6. (Currently amended) The composition of claim 5, wherein ~~the~~^a suppression efficiency of the glutamyl-tRNA synthetase and the glutamyl O-tRNA together is 4 to 5-fold greater than ~~a~~^{the} suppression efficiency of the glutamyl O-tRNA in the absence of the glutamyl-tRNA synthetase.

7. (Cancelled)

8. (Currently amended) The composition of claim 5, wherein the RS glutamyl-tRNA synthetase comprises an amino acid sequence comprising any one of SEQ ID NO.: 69 (*AfRS*), SEQ ID NO.: 73 (*MmRS*), SEQ ID NO.: 75 (*MtRS*), or SEQ ID NO.: 77 (*PhRS*).

9. (Cancelled)

10. (Cancelled)

11. (Cancelled)

12. (Original) The composition of claim 1, comprising a cell.

13. (Original) The composition of claim 12, wherein the cell is an *E. coli* cell.

14. (Original) The composition of claim 1, comprising a translation system.

15. (Currently amended) A cell comprising a translation system, wherein the translation system comprises:

an orthogonal glutamyl-tRNA (glutamyl O-tRNA), ~~derived from one or more archaeal tRNAs, wherein the glutamyl O-tRNA comprising~~es a polynucleotide sequence at least 95%~~80%~~ identical to SEQ ID NO.: 67, ~~wherein the glutamyl O-tRNA comprises a G:C base pair at positions corresponding to 10:28;~~

a glutamyl-tRNA synthetase derived from an RS selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosa*~~cina~~ *mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase; and,

a first selected amino acid;

wherein the glutamyl O-tRNA recognizes a first selector codon, and the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with the first selected amino acid.

16. (Cancelled)

17. (Currently amended) The cell of claim 15, wherein the glutamyl O-tRNA comprises or is transcribed from~~needed by~~ a polynucleotide sequence as set forth in SEQ ID NO.: 67 and a complementary polynucleotide sequence thereof, and wherein the glutamyl-tRNA synthetase comprises an amino acid sequence as set forth in any one of SEQ ID NO.: 69 (A/RS), SEQ ID NO.: 73 (MmRS), SEQ ID NO.: 75 (MtRS), or SEQ ID NO.: 77 (PhRS).

18. (Previously presented) The cell of claim 15, wherein the cell further comprises an additional different O-tRNA/tRNA synthetase pair and a second selected amino acid, wherein the additional O-tRNA recognizes a second selector codon and the additional tRNA synthetase preferentially aminoacylates the additional O-tRNA with the second selected amino acid.

19. (Cancelled)

20. (Original) The cell of claim 15, wherein the cell is a non-eukaryotic cell.

21. (Original) The cell of claim 20, wherein the non-eukaryotic cell is an *E. coli* cell.

22. (Original) The cell of claim 15, further comprising a nucleic acid that comprises a polynucleotide that encodes a polypeptide of interest, wherein the polynucleotide comprises a selector codon that is recognized by the glutamyl O-tRNA.

23. (Currently amended) An *E. coli* cell, comprising:
an orthogonal glutamyl tRNA (glutamyl O-tRNA), wherein the glutamyl O-tRNA comprises a polynucleotide sequence at least 95%~~80%~~ identical to SEQ ID NO.: 67, wherein the glutamyl O-tRNA comprises a G:C base pair at positions corresponding to 10:28;
a glutamyl-tRNA synthetase, wherein the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid;
the selected amino acid; and,
a nucleic acid that comprises a polynucleotide that encodes a polypeptide of interest, wherein the polynucleotide comprises the selector codon that is recognized by the glutamyl O-tRNA, and wherein the glutamyl O-tRNA is derived from one or more archaeal tRNAs

Appl. No. 10/563,656
Response Dated October 8, 2008
Reply to Office Action of July 9, 2008

and the glutamyl-tRNA synthetase comprises at least 90% identity to ~~is derived from an~~
glutamyl-RS selected from the group consisting of: an *Archaeoglobus fulgidus (Af)*
synthetase SEQ ID NO.: 69, a *Methanosa**r**cina maz**e**i* (*Mm*) synthetase SEQ ID NO.: 73, a
Methanobacterium thermoautotrophicum (Mt) synthetase SEQ ID NO.: 75, and a
Pyrococcus horikoshii (Ph) synthetase SEQ ID NO.: 77.